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1: NP_660187. ATP-binding cassette...[gi:21729876]

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LOCUS NP_660187 1344 aa linear PRI 07-SEP-2003
 DEFINITION ATP-binding cassette, sub-family C, member 11 isoform b; multi-resistance protein 8; ATP-binding cassette transporter MRP8; ATP-binding cassette protein C11 [Homo sapiens].
 ACCESSION NP_660187
 VERSION NP_660187.1 GI:21729876
 DBSOURCE REFSEQ: accession NM_145186.1
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 1344)
 AUTHORS Turriziani,O., Schuetz,J.D., Focher,F., Scagnolari,C., Sampath,J., Adachi,M., Bambacioni,F., Riva,E. and Antonelli,G.
 TITLE Impaired 2',3'-dideoxy-3'-thiacytidine accumulation in T-lymphoblastoid cells as a mechanism of acquired resistance independent of multidrug resistant protein 4 with a possible role for ATP-binding cassette C11
 JOURNAL Biochem. J. 368 (Pt 1), 325-332 (2002)
 MEDLINE 22304623
 PUBMED 12133003
 REMARK GeneRIF: Impaired 2',3'-dideoxy-3'-thiacytidine accumulation in T-lymphoblastoid cells as a mechanism of acquired resistance independent of multidrug resistant protein 4 with a possible role for ATP-binding cassette C11.
 REFERENCE 2 (residues 1 to 1344)
 AUTHORS Yabuuchi,H., Shimizu,H., Takayanagi,S. and Ishikawa,T.
 TITLE Multiple splicing variants of two new human ATP-binding cassette transporters, ABCC11 and ABCC12
 JOURNAL Biochem. Biophys. Res. Commun. 288 (4), 933-939 (2001)
 MEDLINE 21547789
 PUBMED 11688999
 REMARK GeneRIF: alternative splice variants and gene expression
 REFERENCE 3 (residues 1 to 1344)
 AUTHORS Bera,T.K., Lee,S., Salvatore,G., Lee,B. and Pastan,I.
 TITLE MRP8, a new member of ABC transporter superfamily, identified by EST database mining and gene prediction program, is highly expressed in breast cancer
 JOURNAL Mol. Med. 7 (8), 509-516 (2001)
 MEDLINE 21475973
 PUBMED 11591886
 REFERENCE 4 (residues 1 to 1344)
 AUTHORS Tammur,J., Prades,C., Arnould,I., Rzhetsky,A., Hutchinson,A., Adachi,M., Schuetz,J.D., Swoboda,K.J., Ptacek,L.J., Rosier,M., Dean,M. and Allikmets,R.
 TITLE Two new genes from the human ATP-binding cassette transporter

superfamily, ABCC11 and ABCC12, tandemly duplicated on chromosome 16q12
JOURNAL Gene 273 (1), 89-96 (2001)
MEDLINE 21376129
PUBMED 11483364
REFERENCE 5 (residues 1 to 1344)
AUTHORS Dean, M., Rzhetsky, A. and Allikmets, R.
TITLE The human ATP-binding cassette (ABC) transporter superfamily
JOURNAL Genome Res. 11 (7), 1156-1166 (2001)
MEDLINE 21329047
PUBMED 11435397
COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AF411579.1.

Summary: The protein encoded by this gene is a member of the superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intra-cellular membranes. ABC genes are divided into seven distinct subfamilies (ABC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This ABC full transporter is a member of the MRP subfamily which is involved in multi-drug resistance. It is expressed at low levels in all tissues, except kidney, spleen, and colon. This gene and family member ABCC12 are determined to be derived by duplication and are both localized to chromosome 16q12.1. Their chromosomal localization, potential function, and expression patterns identify them as candidates for paroxysmal kinesigenic choreoathetosis, a disorder characterized by attacks of involuntary movements and postures, chorea, and dystonia. Multiple alternatively spliced transcript variants have been described for this gene.

Transcript Variant: This variant (3) lacks an alternate in-frame exon compared to variant 1, resulting in a shorter protein (isoform b), compared to isoform a.

FEATURES	Location/Qualifiers
source	1..1344 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="16" /map="16q12.1"
<u>Protein</u>	1..1344 /product="ATP-binding cassette, sub-family C, member 11 isoform b" /note="multi-resistance protein 8; ATP-binding cassette transporter MRP8; ATP-binding cassette protein C11"
<u>Region</u>	150..732 /region_name="ABC-type multidrug transport system, ATPase and permease components [Defense mechanisms]" /note="MdlB" /db_xref="CDD: <u>COG1132</u> "
<u>Region</u>	853..1338 /region_name="ABC-type multidrug transport system, ATPase and permease components [Defense mechanisms]" /note="MdlB" /db_xref="CDD: <u>COG1132</u> "
CDS	1..1344 /gene="ABCC11" /coded_by="NM_145186.1:79..4113" /db_xref="LocusID:85320" /db_xref="MIM:607040"

ORIGIN

1 mtrkrtywvp nssgglnvrg fdigddmvsg liykttytlqd gpwsqqernp eapgraavpp
61 wkydaalrt mipfrpkprf papqpldnag lfsyltvswl tplmiqslrs rldentippl
121 svhdasdknv qrlhrlweee vssrrgiekas vllvmlrfqr trlifdallg icfciasvlg
181 piliipkile yseeqlgnvv hvgglcfalf lsecvkslsf ssswiinqrt airfraavss
241 fafekliqfk svihitsgea isfftgdvny 1fegvcygpl vlitcaslvi csissyfiig
301 ytafiaiacy l1vfplavfm trmavkagh tsevsdqrrir vtsevltcik likmytwekp
361 fakiedlrr kerklllekcg lvqsltsitl fiiptvatav wlihtslkl kltasmafsm
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481 lswqqtcpgi vngalelern ghasegmtrp rdalgpeeg nslgpelhki nlvvskgmml
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721 qkkgkyaqli qkmhkeatsd mlqdtakiae kpkvesqala tsleeslgn avpehqltqe
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841 resngtmadl gniadnpqls fyqlvyglna lllicvgvcs s giftkvtrk astalhnklf
901 nkvfrcpmsf fdtipigrl1 ncfagdleql dqllpifseq flvlslmvia vllivsvlsp
961 yillmgaiim vicfiyymmf kkaigvfkrl enysrsplfs hilnslqgls sihvygktd
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1141 iifqdyhmky rdntptvlhg intirghev vgivgrtgsg ksslgmalfr lvepmagril
1201 idgvdicsig ledlrskslv ipqdpvllsg tirfnldpfh rhtdqqiwdl lertfltkai
1261 ilideatasi dmetdtliqr tireafqgct vlviahrvtt vlncdhilvm gngkvvefdr
1321 pevrlkkpgs lfaalmatat ssr

//

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Sep 4 2003 10:24:36

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaGAABJayWj: 1219 aa
>seqid24
vs /tmp/fastaAACJayWj library
searching /tmp/fastaAACJayWj library

1344 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 40, opt: 28, gap-pen: -12/ -2, width: 16
Scan time: 0.034

The best scores are:

NP_660187 ACCESSION:NP_660187 NID: gi 21729876 re (1344) 4838

opt

>>NP_660187 ACCESSION:NP_660187 NID: gi 21729876 ref NP_ (1344 aa)

initn: 7156 init1: 4838 opt: 4838

Smith-Waterman score: 7274; 85.311% identity in 1382 aa overlap (1-1219:1-1344)

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NP_660 MTRKRTYWVNPNSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::

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NP_660 WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTWSLTPLMIQSLRSRLDENTIPPL	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::

70	80	90	100	110	120
seqid2 WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTWSLTPLMIQSLRSRLDENTIPPL	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
NP_660 WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTWSLTPLMIQSLRSRLDENTIPPL	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::

130	140	150	160	170	180
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130	140	150	160	170	180
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190	200	210	220	230	240
seqid2 PILIIPKILEYSEEQLGVVHGVLGFALFSECVKSLSFSSSWIINQRTAIRFQAAVSS	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::
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370 380 390 400 410 420

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